STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 139767

TO: James Schultz **Location: REM/2D18/2C18** **Art Unit: 1635** **Wednesday, December 08, 2004** **Case Serial Number: 09/913800**	**From: David Schreiber** **Location: Biotech-Chem Library** **Remsen E01A61** **Phone: 272-2526** **david.schreiber@uspto.gov**

Search Notes

Access DB# _____

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner # : _____ Date: _____
Art Unit: _____ Phone Number 30_____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

****

STAFF USE ONLY	Type of Search		Vendors and cost where applicable	
Searcher: P. Schreiber	NA Sequence (#)	22	STN	
Searcher Phone #: 272-2526	AA Sequence (#)		Dialog	
Searcher Location: Remsen E01/4G1	Structure (#)		Questel/Orbit	
Date Searcher Picked Up:	Bibliographic		Dr.Link	
Date Completed: 12/8	Litigation		Lexis/Nexis	
Searcher Prep & Review Time: 15	Fulltext		Sequence Systems	Compugen
Clerical Prep Time:	Patent Family		WWW/Internet	
Online Time: 126	Other		Other (specify)	

PTO-1590 (8-01)

139767

Schreiber, David

From: Schultz, James
Sent: Wednesday, November 17, 2004 10:09 AM
To: Schreiber, David
Subject: Score over length search 09/913,800

Hi David,
I need a score over length nucleotide sequence search on SEQ ID NOS: 32 and 21 in the above entitled case. I need the lower and upper limits to be 8 and 30, respectively, I only need hits that are 100% complementary, and please transfer as many hits into the excel program as possible. No need to search the interference databases at this time.

I realize you don't normally search more than two sequences, but applicants have asserted that these two sequences are usable together, and that they both comprise the invention...I don't see any way around searching these.

Also, can you give me an idea how long it is typically taking to get results back these days for this type of search?

Thanks,
Doug Schultz

James Douglas Schultz, PhD
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 100 %.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:35:33 ; Search time 0.001 Seconds
(without alignments)
1.908 Million cell updates/sec

Title: US-09-913-800-21
Perfect score: 18
Sequence: 1 cttgaggctgttggcgac 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 5 seqs, 53 residues

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 5 summaries

Database : rng21.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	1	AAA08468	Human Akt-2 phosph
2	9	50.0	9	1	ABQ72180	Zinc finger protei
3	9	50.0	9	1	ADA64507	Zinc finger target
4	9	50.0	9	1	ADM23199	Synthetic zinc fin
5	8	44.4	8	1	AAA80787	A. thaliana primer

ALIGNMENTS

RESULT 1
AAA08468
ID AAA08468 standard; DNA; 18 BP.
XX
AC AAA08468;
XX
DT 17-JUL-2000 (first entry)
XX
DE Human Akt-2 phosphorothioate antisense oligonucleotide SEQ ID NO:21.
XX
KW Human; Akt-2; antisense oligonucleotide; phosphorothioate; inhibition;
KW serine/threonine kinase; antiinflammatory; cytostatic; antiifectious;
KW gene therapy; infection; inflammation; tumour; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .18
FT /*tag= a
FT /note= "phosphorothioate linkages"
XX
PN US6043090-A.
XX
PD 28-MAR-2000.
XX
PF 23-FEB-1999; 99US-00256465.
XX
PR 23-FEB-1999; 99US-00256465.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowsert LM;
XX
DR WPI; 2000-270345/23.
XX
PT Antisense compound for diagnosis and treatment of infection, inflammation
PT and tumor formation is targeted towards the nucleic acid encoding a
PT member of serine/threonine family of kinases.
XX
PS Claim 3; Col 38; 30pp; English.
XX
CC The present invention describes antisense compounds of about 8-30
CC nucleotides in length targeted to the 5' UTR (untranslated region), 3'
CC UTR or coding region of the nucleic acid encoding human Akt-2, which
CC inhibits the expression of human AKT-2. Human Akt-2 is a member of the
CC Akt/PKB family of serine/threonine kinases. The antisense compounds have
CC antiinflammatory, cytostatic and antiifectious activities, and can be
CC used in gene therapy. They are useful in inhibiting the expression of
CC human Akt-2 by contacting the cells or the tissues in vitro. They can
CC also be used for diagnosis and treatment of infection, inflammation and
CC tumour formation, and for prophylaxis. The present sequence represents a
CC human Akt-2 phosphorothioate antisense oligonucleotide used in the
CC exemplification of the present invention
XX
SQ Sequence 18 BP; 2 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTGAGGCTGTTGGCGAC 18
              ||||||||||||||||||
Db          1 CTTGAGGCTGTTGGCGAC 18
```

RESULT 2
ABQ72180
ID ABQ72180 standard; DNA; 9 BP.
XX
AC ABQ72180;
XX
DT 28-AUG-2002 (first entry)
XX
DE Zinc finger protein related oligonucleotide target SEQ ID NO:2478.
XX
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200242459-A2.
XX
PD 30-MAY-2002.
XX
PF 20-NOV-2001; 2001WO-US043438.
XX
PR 20-NOV-2000; 2000US-00716637.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Liu Q;
XX
DR WPI; 2002-500284/53.
XX
PT New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises

PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
PS Example 1; Page 63; 81pp; English.
XX
CC The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target subsite. Also described are: (1) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
CC binds to the S2 target subsite, and selecting the F3 zinc finger such
CC that it binds to the S3 target subsite, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target subsites
CC having the nucleotide G in the 5'-most position of the subsite. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determined the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. ABQ71213 to
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
XX
SQ Sequence 9 BP; 1 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

```
  Query Match             50.0%;  Score 9;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GAGGCTGTT 12
              |||||||||
Db          1 GAGGCTGTT 9
```

RESULT 3
ADA64507
ID ADA64507 standard; DNA; 9 BP.
XX
AC ADA64507;
XX
DT 20-NOV-2003 (first entry)
XX
DE Zinc finger target sequence DNA #965.
XX
KW ds; target sequence; zinc finger protein;
KW multi-finger zinc finger protein; improved affinity;
KW improved specificity; enhanced biological activity.
XX
OS Synthetic.
XX
PN US2003068675-A1.
XX
PD 10-APR-2003.
XX
PF 20-NOV-2001; 2001US-00990186.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
DR WPI; 2003-567233/53.
XX
PT Designing zinc finger protein that has three zinc fingers from N-terminus
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
PT site, by selecting zinc fingers that bind their respective subsites.
XX
PS Disclosure; Page 27; 34pp; English.
XX
CC The invention relates to a method of designing a zinc finger protein. The
CC method is useful for designing a zinc finger protein. The method provides
CC multi-finger zinc finger proteins with improved affinity and specificity
CC for their target sequences, as well as enhanced biological activity. The
CC present sequence represents a zinc finger protein DNA target sequence.
XX
SQ Sequence 9 BP; 1 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

```
  Query Match             50.0%;  Score 9;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GAGGCTGTT 12
              |||||||||
Db          1 GAGGCTGTT 9
```

RESULT 4
ADM23199
ID ADM23199 standard; DNA; 9 BP.
XX
AC ADM23199;
XX
DT 20-MAY-2004 (first entry)
XX
DE Synthetic zinc finger protein target DNA #965.
XX
KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX
OS Unidentified.
XX
PN US2003104526-A1.
XX
PD 05-JUN-2003.
XX
PF 20-NOV-2001; 2001US-00989994.
XX
PR 24-MAR-1999; 99US-0126238P.
PR 24-MAR-1999; 99US-0126239P.
PR 30-JUL-1999; 99US-0146595P.
PR 30-JUL-1999; 99US-0146615P.
PR 23-MAR-2000; 2000US-00535008.
PR 20-NOV-2000; 2000US-00716637.
XX
PA (LIUQ/) LIU Q.
XX
PI Liu Q;
XX
DR WPI; 2003-843091/78.
XX
PT New zinc finger protein used for recognizing triplet target subsites
PT having nucleotide G in 5'-most position of subsite, that has been
PT optimized with respect to location of subsite within target site.
XX
PS Example 6; SEQ ID NO 2478; 48pp; English.
XX
CC The invention describes a new zinc finger protein that binds to a target
CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
CC (S3) target subsites. The zinc finger proteins can be used for
CC recognising triplet target subsites having the nucleotide G in the 5'-
CC most position of the subsite, that has been optimised with respect to the
CC location of the subsite within the target site. This sequence represents
CC the target polynucleotide to which the zinc finger protein sp-1 consensus
CC sequence binds.
XX

```
SQ   Sequence 9 BP; 1 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             50.0%;  Score 9;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GAGGCTGTT 12
              |||||||||
Db          1 GAGGCTGTT 9


RESULT 5
AAA80787
ID   AAA80787 standard; DNA; 8 BP.
XX
AC   AAA80787;
XX
DT   24-NOV-2000  (first entry)
XX
DE   A. thaliana primer walking octamer SEQ ID NO: 100.
XX
KW   Primer walking; octamer; primer; DNA sequencing; PCR; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US6083695-A.
XX
PD   04-JUL-2000.
XX
PF   21-MAY-1997;   97US-00859954.
XX
PR   15-APR-1996;   96US-00632782.
XX
PA   (UYHO-) UNIV HOUSTON.
PA   (HARD/) HARDIN S H.
XX
PI   Hardin PE,  Hardin SH,  Homayouni R; .
XX
DR   WPI; 2000-474852/41.
XX
PT   Sequencing an unknown DNA molecule for the polymerase chain reaction and
PT   other primer processes comprises primer walking of octamer
PT   oligonucleotides.
XX
PS   Example 8; Col 75-76; 161pp; English.
XX
CC   This invention describes a novel method for sequencing an unknown DNA
CC   molecule which comprises selecting a library primer from an octamer
CC   oligonucleotide library consisting of 48 8-bp sequences and corresponding
CC   complementary sequences, where the library primer is complementary to a
CC   known sequence adjacent to the unknown sequence or is complementary to a
CC   sequence in a known extension product. The method is useful for DNA
CC   nucleotide sequencing, in PCR, and in other processes which make use of
CC   primers. The octamers are used to identify coding sequences. Primer
CC   walking using the octamer libraries is advantageous over other sequencing
CC   methods because it does not require multiple cloning steps nor subsequent
CC   template preparations, and it is a directed and methodical approach.
CC   AAA80688-A81253 represent the octamer primers used in the primer walking
CC   method of the invention
XX
SQ   Sequence 8 BP; 1 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             44.4%;  Score 8;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TTGAGGCT 9
              ||||||||
Db          1 TTGAGGCT 8


Search completed: December  8, 2004, 06:35:34
Job time : 0.001 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:38:09 ; Search time 0.001 Seconds
(without alignments)
0.972 Million cell updates/sec

Title: US-09-913-800-21
Perfect score: 18
Sequence: 1 cttgaggctgttggcgac 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 3 seqs, 27 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database : rnpb21.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	50.0	9	1	US-09-989-789-2478	Sequence 2478, Ap
2	9	50.0	9	1	US-09-990-186-2478	Sequence 2478, Ap
3	9	50.0	9	1	US-09-989-994-2478	Sequence 2478, Ap

ALIGNMENTS

RESULT 1
US-09-989-789-2478
; Sequence 2478, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2478
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-2478

Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 GAGGCTGTT 12
              |||||||||
Db          1 GAGGCTGTT 9
```

RESULT 2
US-09-990-186-2478
; Sequence 2478, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2478
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-2478

Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 GAGGCTGTT 12
              |||||||||
Db          1 GAGGCTGTT 9
```

RESULT 3
US-09-989-994-2478
; Sequence 2478, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2478
; LENGTH: 9
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-2478

Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 GAGGCTGTT 12
              |||||||||
Db          1 GAGGCTGTT 9
```

Search completed: December 8, 2004, 06:38:10
Job time : 1 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:41:41 ; Search time 0.001 Seconds
(without alignments)
0.360 Million cell updates/sec

Title: US-09-913-800-32
Perfect score: 18
Sequence: 1 gtgagcgacttcatcctt 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 10 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : rge32.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	10	55.6	10	1	BD239875	ACCESSION:BD239875

ALIGNMENTS

RESULT 1
BD239875/c
LOCUS BD239875 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239875
VERSION BD239875.1 GI:33049645
KEYWORDS JP 2002534056-A/1293.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1293 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/1293
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1. .10
FT /organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
source 1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 55.6%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 TGAGCGACTT 11
              ||||||||||
Db         10 TGAGCGACTT 1
```

Search completed: December 8, 2004, 06:41:41
Job time : 0.001 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:43:02 ; Search time 0.001 Seconds
(without alignments)
1.008 Million cell updates/sec

Title: US-09-913-800-32
Perfect score: 18
Sequence: 1 gtgagcgacttcatcctt 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 28 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : rng32.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	1	AAA08479	Human Akt-2 phosph
c 2	10	55.6	10	1	AAZ78865	Human dendritic ce

ALIGNMENTS

RESULT 1
AAA08479
ID AAA08479 standard; DNA; 18 BP.
XX
AC AAA08479;
XX
DT 17-JUL-2000 (first entry)
XX
DE Human Akt-2 phosphorothioate antisense oligonucleotide SEQ ID NO:32.
XX
KW Human; Akt-2; antisense oligonucleotide; phosphorothioate; inhibition;
KW serine/threonine kinase; antiinflammatory; cytostatic; antiifectious;
KW gene therapy; infection; inflammation; tumour; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1. .18
FT /*tag= a
FT /note= "phosphorothioate linkages"
XX
PN US6043090-A.
XX
PD 28-MAR-2000.
XX
PF 23-FEB-1999; 99US-00256465.
XX
PR 23-FEB-1999; 99US-00256465.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowsert LM;
XX
DR WPI; 2000-270345/23.
XX
PT Antisense compound for diagnosis and treatment of infection, inflammation
PT and tumor formation is targeted towards the nucleic acid encoding a
PT member of serine/threonine family of kinases.
XX
PS Claim 3; Col 38; 30pp; English.
XX
CC The present invention describes antisense compounds of about 8-30
CC nucleotides in length targeted to the 5' UTR (untranslated region), 3'
CC UTR or coding region of the nucleic acid encoding human Akt-2, which
CC inhibits the expression of human AKT-2. Human Akt-2 is a member of the
CC Akt/PKB family of serine/threonine kinases. The antisense compounds have
CC antiinflammatory, cytostatic and antiifectious activities, and can be
CC used in gene therapy. They are useful in inhibiting the expression of
CC human Akt-2 by contacting the cells or the tissues in vitro. They can
CC also be used for diagnosis and treatment of infection, inflammation and
CC tumour formation, and for prophylaxis. The present sequence represents a
CC human Akt-2 phosphorothioate antisense oligonucleotide used in the
CC exemplification of the present invention
XX
SQ Sequence 18 BP; 3 A; 5 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGCGACTTCATCCTT 18
||||||||||||||||||
Db 1 GTGAGCGACTTCATCCTT 18

RESULT 2
AAZ78865/c
ID AAZ78865 standard; DNA; 10 BP.
XX
AC AAZ78865;
XX
DT 10-APR-2000 (first entry)
XX
DE Human dendritic cell SAGE tag, SEQ ID NO:1293.
XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
PN WO9965924-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013800.
XX
PR 19-JUN-1998; 98US-0089833P.
PR 19-JUN-1998; 98US-0089844P.
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089878P.
PR 19-JUN-1998; 98US-0089991P.
PR 19-JUN-1998; 98US-0089992P.
PR 19-JUN-1998; 98US-0089993P.
PR 19-JUN-1998; 98US-0089994P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0089999P.
PR 19-JUN-1998; 98US-0090000P.

PR 19-JUN-1998; 98US-0090035P.
PR 19-JUN-1998; 98US-0090036P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
PR 19-JUN-1998; 98US-0090042P.
PR 19-JUN-1998; 98US-0090043P.
PR 19-JUN-1998; 98US-0090044P.
PR 19-JUN-1998; 98US-0090045P.
PR 19-JUN-1998; 98US-0090047P.
PR 19-JUN-1998; 98US-0090048P.
PR 19-JUN-1998; 98US-0090072P.
PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106077/09.
XX
PT Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
XX
PS Claim 1; Page 102; 130pp; English.
XX
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 55.6%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGAGCGACTT 11
||||||||||
Db 10 TGAGCGACTT 1

Search completed: December 8, 2004, 06:43:02
Job time : 0.001 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:44:34 ; Search time 0.001 Seconds
(without alignments)
0.648 Million cell updates/sec

Title: US-09-913-800-32
Perfect score: 18
Sequence: 1 gtgagcgacttcatcctt 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 18 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : rni32.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	1	US-09-256-465-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-256-465-32
; Sequence 32, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 32
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-256-465-32

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTGAGCGACTTCATCCTT 18
              ||||||||||||||||||
Db          1 GTGAGCGACTTCATCCTT 18
```

Search completed: December 8, 2004, 06:44:34
Job time : 0.001 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:45:59 ; Search time 0.001 Seconds
(without alignments)
0.360 Million cell updates/sec

Title: US-09-913-800-32
Perfect score: 18
Sequence: 1 gtgagcgacttcatcctt 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 10 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : rnpb32.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	10	55.6	10	1	US-10-033-145-1293	Sequence 1293, Ap

ALIGNMENTS

RESULT 1
US-10-033-145-1293/c
; Sequence 1293, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1293
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1293

Query Match 55.6%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 TGAGCGACTT 11
              ||||||||||
Db         10 TGAGCGACTT 1
```

Search completed: December 8, 2004, 06:46:00
Job time : 0.001 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:36:40 ; Search time 0.001 Seconds
(without alignments)
0.936 Million cell updates/sec

Title: US-09-913-800-21
Perfect score: 18
Sequence: 1 cttgaggctgttggcgac 18
Ctt9AGGGAGTT
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 26 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : rni21.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	100.0	18	1	US-09-256-465-21	Sequence 21, Appl
2	8	44.4	8	1	US-08-859-954-100	Sequence 100, App

ALIGNMENTS

RESULT 1
US-09-256-465-21
; Sequence 21, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-256-465-21

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTTGAGGCTGTTGGCGAC 18
              ||||||||||||||||||
Db          1 CTTGAGGCTGTTGGCGAC 18
```

RESULT 2
US-08-859-954-100
; Sequence 100, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-859-954-100

Query Match 44.4%; Score 8; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 TTGAGGCT 9
              ||||||||
Db          1 TTGAGGCT 8
```

Search completed: December 8, 2004, 06:36:41
Job time : 1 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 8, 2004, 06:34:24 ; Search time 0.001 Seconds
(without alignments)
0.324 Million cell updates/sec

Title: US-09-913-800-21
Perfect score: 18
Sequence: 1 cttgaggctgttggcgac 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 9 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 8
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : rge21.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	50.0	9	1	AX669029	ACCESSION:AX669029

ALIGNMENTS

RESULT 1
AX669029
LOCUS AX669029 9 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 2478 from Patent WO0242459.
ACCESSION AX669029
VERSION AX669029.1 GI:29292006
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc fingers
JOURNAL Patent: WO 0242459-A 2478 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES Location/Qualifiers
source 1. .9
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="example target DNA"

Query Match 50.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 GAGGCTGTT 12
              |||||||||
Db          1 GAGGCTGTT 9
```

Search completed: December 8, 2004, 06:34:24
Job time : 0.001 secs